

DECLARATION AND POWER OF
ATTORNEY FOR PATENT APPLICATION

Attorney's Docket No. DX0669K

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name;

I believe I am the original, first sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

"ISOLATED MAMMALIAN DENDRITIC CELL GENES: RELATED REAGENTS"

the specification of which

☐ is attached hereto.

☒ was filed on November 26, 1997 as Application Serial No. 08/978,289

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s):	Priority Claimed
-------------------------------	------------------

(Number)

(Country)

(Day/Month/Year Filed)

Yes or No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below:

60/031,806

(Application Number)

November 27, 1996

(Filing Date)

60/032,767

(Application Number)

December 11, 1996

(Filing Date)

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

(Application Serial No.)

(Filing Date)

(Status – patented, pending, abandoned)

Power of Attorney: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in Patent and Trademark Office connected therewith. (List name and registration number.)

Carl W. Battle	Reg. No. 30,731	Anita W. Magatti	Reg. No. 29,825
Edwin P. Ching	Reg. No. 34,090	John J. Maitner	Reg. No. 25,636
Eric S. Dicker	Reg. No. 31,699	Joseph T. Majka	Reg. No. 30,570
Norman C. Dulak	Reg. No. 31,608	Arthur Mann	Reg. No. 35,598
Cynthia L. Foulke	Reg. No. 32,364	Edward H. Mazer	Reg. No. 27,573
Robert A. Franks	Reg. No. 28,605	Jaye P. McLaughlin	Reg. No. 41,211
James M. Gould	Reg. No. 33,702	Richard B. Murphy	Reg. No. 35,298
Richard J. Grochala	Reg. No. 31,518	James R. Nelson	Reg. No. 27,929
Thomas D. Hoffman	Reg. No. 28,221	Immac J. Thampoe	Reg. No. 36,322
Henry C. Jeanette	Reg. No. 30,856	Paul A. Thompson	Reg. No. 35,385
Susan Lee	Reg. No. 30,653	Donald W. Wyatt	Reg. No. 40,879

Send Correspondence to: Edwin P. Ching DNAX Research Institute 901 California Avenue Palo Alto, CA 94304-1104	Direct Telephone Calls to: Name: Edwin P. Ching Telephone No.: (650) 496-1204 Facsimile No.: (650) 496-1200
---	--

FULL NAME OF 1ST OR SOLE INVENTOR	FAMILY NAME Bates	FIRST GIVEN NAME Elizabeth	SECOND GIVEN NAME Esther Mary
RESIDENCE & CITIZENSHIP	CITY Lyon	STATE OR FOREIGN COUNTRY France	COUNTRY OF CITIZENSHIP United Kingdom
POST OFFICE ADDRESS	POST OFFICE ADDRESS 13, rue Terme	CITY Lyon	STATE & ZIP CODE/COUNTRY France 69001

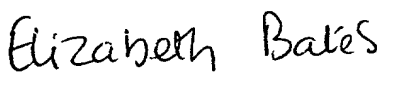


FULL NAME OF 2ND JOINT INVENTOR	FAMILY NAME de Saint-Vis	FIRST GIVEN NAME Blandine	SECOND GIVEN NAME Marie
RESIDENCE & CITIZENSHIP	CITY Lyon	STATE OR FOREIGN COUNTRY France	COUNTRY OF CITIZENSHIP France
POST OFFICE ADDRESS	POST OFFICE ADDRESS 76, rue d'Anvers	CITY Lyon	STATE & ZIP CODE/COUNTRY France 69007

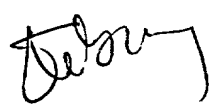
FULL NAME OF 3RD JOINT INVENTOR	FAMILY NAME Caux	FIRST GIVEN NAME Christophe	SECOND GIVEN NAME
RESIDENCE & CITIZENSHIP	CITY France	STATE OR FOREIGN COUNTRY Lyon	COUNTRY OF CITIZENSHIP France
POST OFFICE ADDRESS	POST OFFICE ADDRESS 1, rue de Savoie	CITY Lyon	STATE & ZIP CODE/COUNTRY France 69002

FULL NAME OF 4TH JOINT INVENTOR	FAMILY NAME Lebecque	FIRST GIVEN NAME Serge	SECOND GIVEN NAME J. E.
RESIDENCE & CITIZENSHIP	CITY Civrieux d' Azergue	STATE OR FOREIGN COUNTRY France	COUNTRY OF CITIZENSHIP Belgium
POST OFFICE ADDRESS	POST OFFICE ADDRESS 514. Chemin du Marand	CITY Civrieux d' Azergue	STATE & ZIP CODE/COUNTRY France 69380

FULL NAME OF 5TH JOINT INVENTOR	FAMILY NAME Banchereau	FIRST GIVEN NAME Jacques	SECOND GIVEN NAME .
RESIDENCE & CITIZENSHIP	CITY Dallas	STATE OR FOREIGN COUNTRY Texas	COUNTRY OF CITIZENSHIP France
POST OFFICE ADDRESS	POST OFFICE ADDRESS 2752 Gaston	CITY Dallas	STATE & ZIP CODE/COUNTRY Texas 75226

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Signature of First Inventor 	Signature of Second Inventor 	Signature of Third Inventor 
Elizabeth Esther Mary Bates	Blandine Marie de Saint-Vis	Christophe Caux
Date 13/02/98	Date 16/2/98	Date 13/02/98

Signature of Fourth Inventor 	Signature of Fifth Inventor
Serge J.E. Lebecque	Jacques Banchereau
Date 16/02/1998	Date

FULL NAME OF 4TH JOINT INVENTOR	FAMILY NAME Lebecque	FIRST GIVEN NAME Serge	SECOND GIVEN NAME J. E.
RESIDENCE & CITIZENSHIP	CITY Civrieux d' Azergue	STATE OR FOREIGN COUNTRY France	COUNTRY OF CITIZENSHIP Belgium
POST OFFICE ADDRESS	POST OFFICE ADDRESS 514. Chemin du Marand	CITY Civrieux d' Azergue	STATE & ZIP CODE/COUNTRY France 69380

FULL NAME OF 5TH JOINT INVENTOR	FAMILY NAME Banchereau	FIRST GIVEN NAME Jacques	SECOND GIVEN NAME .
RESIDENCE & CITIZENSHIP	CITY Dallas	STATE OR FOREIGN COUNTRY Texas	COUNTRY OF CITIZENSHIP France
POST OFFICE ADDRESS	POST OFFICE ADDRESS 2752 Gaston	CITY Dallas	STATE & ZIP CODE/COUNTRY Texas 75226

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Signature of First Inventor	Signature of Second Inventor	Signature of Third Inventor
Elizabeth Esther Mary Bates	Blandine Marie de Saint-Vis	Christophe Caux
Date	Date	Date

Signature of Fourth Inventor	Signature of Fifth Inventor
Serge J.E. Lebecque	Jacques Banchereau
Date	Date 28 January 1998.

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is human A05F12 diubiquitin nucleotide sequence.
SEQ ID NO: 2 is human A05F12 diubiquitin polypeptide sequence.
SEQ ID NO: 3 is mouse A05F12 diubiquitin nucleotide sequence.
SEQ ID NO: 4 is mouse A05F12 diubiquitin polypeptide sequence.
SEQ ID NO: 5 is human A07C03 Ig family gene nucleotide sequence.
10 SEQ ID NO: 6 is human A07C03 Ig family gene polypeptide sequence.
SEQ ID NO: 7 is revised human A07C03 Ig family gene nucleotide sequence.
SEQ ID NO: 8 is revised human A07C03 Ig family gene polypeptide sequence.
SEQ ID NO: 9 is mouse A07C03 Ig family gene nucleotide sequence.
SEQ ID NO: 10 is mouse A07C03 Ig family gene polypeptide sequence.
15 SEQ ID NO: 11 is human E02B02 LAMP-like gene nucleotide sequence.
SEQ ID NO: 12 is human E02B02 LAMP-like gene polypeptide sequence.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bates, Elizabeth E.M.
de Saint-Vis, Blandine M.
Caux, Christophe
Lebecque, Serge J.E.
Banchereau, Jacques

(ii) TITLE OF INVENTION: ISOLATED MAMMALIAN DENDRITIC CELL GENES;
RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
40 (F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
45 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
50 (B) FILING DATE: 25-NOV-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,767
55 (B) FILING DATE: 11-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/031,806

(B) FILING DATE: 27-NOV-1996

5

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.

(B) REGISTRATION NUMBER: 34,090

(C) REFERENCE/DOCKET NUMBER: DX0669K

10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196

(B) TELEFAX: (650)496-1204

15

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 19..513

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCTTGT CTGCAGAG ATG GCT CCC AAT GCT TCC TGC CTC TGT GTG CAT 51
Met Ala Pro Asn Ala Ser Cys Leu Cys Val His
1 5 10

GTC CGT TCC GAG GAA TGG GAT TTA ATG ACC TTT GAT GCC AAC CCA TAT 99
Val Arg Ser Glu Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr
15 20 25

GAC AGC GTG AAA AAA ATC AAA GAA CAT GTC CGG TCT AAG ACC AAG GTT 147
Asp Ser Val Lys Lys Ile Lys Glu His Val Arg Ser Lys Thr Lys Val
30 35 40

CCT GTG CAG GAC CAG GTT CTT TTG CTG GGC TCC AAG ATC TTA AAG CCA 195
Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro
45 50 55

CGG AGA AGC CTC TCA TCT TAT GGC ATT GAC AAA GAG AAG ACC ATC CAC 243
Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His
60 65 70 75

CTT ACC CTG AAA GTG GTG AAG CCC AGT GAT GAG GAG CTG CCC TTG TTT 291
Leu Thr Leu Lys Val Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe
80 85 90

55

CTT GTG GAG TCA GGT GAT GAG GCA AAG AGG CAC CTC CTC CAG GTG CGA 339
 Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg
 95 100 105
 5
 AGG TCC AGC TCA GTG GCA CAA GTG AAA GCA ATG ATC GAG ACT AAG ACG 387
 Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr
 110 115 120
 10
 GGT ATA ATC CCT GAG ACC CAG ATT GTG ACT TGC AAT GGA AAG AGA CTG 435
 Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu
 125 130 135
 15
 GAA GAT GGG AAG ATG ATG GCA GAT TAC GGC ATC AGA AAG GGC AAC TTA 483
 Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu
 140 145 150 155
 CTC TTC CTG GCA TCT TAT TGT ATT GGA GGG TGACCACCCT GGGGATGGGG 533
 Leu Phe Leu Ala Ser Tyr Cys Ile Gly Gly
 160 165
 20
 TGT TGGCAGG GGTCAAAAAG CTTATTTCTT TTAATCTCTT ACTCAACGAA CACATCTTCT 593
 25
 GATGATTTCC CAAAATTAAT GAGAATGAGA TGAGTAGAGT AAGATTTGGG TGGGATGGGT 653
 AGGATGAAGT ATATTGCCCA ACTCTATGTT TCTTTGATTC TAACACAATT AATTAAGTGA 713
 CATGATTTTT ACTAATGTAT TACTGAGACT AGTAAATAAA TTTTAAAGGC AAAATAGAGC 773
 30
 ATTC 777

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
 1 5 10 15
 Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
 20 25 30
 Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
 35 40 45
 Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
 50 55 60

Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65 70 75 80

Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
85 90 95

Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
100 105 110

Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
115 120 125

Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
130 135 140

Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145 150 155 160

Tyr Cys Ile Gly Gly
165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACAGAC ATG GCT TCT GTC CGC ACC TGT GTT GTC CGT TCA GAC CAA TGG 49
Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp
1 5 10

CGG TTA ATG ACC TTT GAG ACC ACT GAG AAT GAC AAA GTG AAG AAG ATA 97
Arg Leu Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile
15 20 25 30

AAT GAA CAT ATT AGG TCC CAA ACC AAG GTC TCT GTA CAG GAC CAG ATC 145
Asn Glu His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile
35 40 45

CTT CTG CTA GAC TCC AAA ATC CTC AAG CCC CAT CGA AAA TTG TCA TCC 193
Leu Leu Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser
50 55 60

TAT GGG ATT GAC AAG GAA ACC ACT ATC CAC CTT ACC CTG AAG GTG GTG 241
Tyr Gly Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val
65 70 75

5 AAG CCC AGT GAT GAA GAG CTG CCC TTG TTT CTG GTG GAG TCC AAA AAC 289
Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn
80 85 90

10 GAG GGG CAA AGG CAC CTC CTC CGA GTT CGA AGA TCC AGC TCA GTG GCC 337
Glu Gly Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala
95 100 105 110

15 CAG GTG AAA GAG ATG ATC GAG AGT GTG ACC TCT GTG ATC CCT AAG AAG 385
Gln Val Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys
115 120 125

CAG GTT GTG AAT TGC AAC GGA AAG AAG CTG GAA GAT GGA AAG ATC ATG 433
Gln Val Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met
130 135 140

20 GCT GAC TAC AAC ATC AAG AGT GGC AGT TTG CTC TTT CTG ACA ACA CAC 481
Ala Asp Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His
145 150 155

25 TGC ACT GGG GGA TGA 496
Cys Thr Gly Gly
160

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp Arg Leu
1 5 10 15

Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile Asn Glu
20 25 30

His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile Leu Leu
35 40 45

Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser Tyr Gly
50 55 60

Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val Lys Pro
65 70 75 80

Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn Glu Gly
85 90 95

Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala Gln Val
100 105 110

Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys Gln Val
115 120 125

Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met Ala Asp
130 135 140

Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His Cys Thr
145 150 155 160

Gly Gly

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1040 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 45..767

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 111..767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG 56
Met Gly Thr Ala
-22 -20

AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT 104
Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe
-15 -10 -5

TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG 152
Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp
1 5 10

TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC 200
Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr
15 20 25 30

TTC TCC GCA ACC GGA TGC CCT TCT GAG CAA CCA ACA TGC CTG TGG TTT 248
 Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr Cys Leu Trp Phe
 35 40 45

CGC TAC GGT GCT CAC CAG CCT GAG AAC CTG TGC TTG GAC GGG TGC AAA 296
 Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu Asp Gly Cys Lys
 50 55 60

AGT GAG GCA GAC AAG TTC ACA GTG AGG GAG GCC CTC AAA GAA AAC CAA 344
 Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu Lys Glu Asn Gln
 65 70 75

GTT TCC CTC ACT GTA AAC AGA GTG ACT TCA AAT GAC AGT GCA ATT TAC 392
 Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp Ser Ala Ile Tyr
 80 85 90

ATC TGT GGA ATA GCA TTC CCC AGT GTG CCG GAA GCG AGA GCT AAA CAG 440
 Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala Arg Ala Lys Gln
 95 100 105 110

ACA GGA GGA GGG ACC ACA CTG GTG GTA AGA GAA ATT AAG CTG CTC AGC 488
 Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile Lys Leu Leu Ser
 115 120 125

AAG GAA CTG CGG AGC TTC CTG ACA GCT CTT GTA TCA CTG CTC TCT GTC 536
 Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser Leu Leu Ser Val
 130 135 140

TAT GTG ACC GGT GTG TGC GTG GCC TTC ATA CTC CTC TCC AAA TCA AAA 584
 Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu Ser Lys Ser Lys
 145 150 155

TCC AAC CCT CTA AGA AAG AAA GAA ATA AAA GAA GAC TCA CAA AAG AAG 632
 Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp Ser Gln Lys Lys
 160 165 170

AAG AGT GCT CGG CGT ATT TTT CAG GAA ATT GCT CAA GAA CTA TAC CAT 680
 Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu Tyr His
 175 180 185 190

AAG AGA CAT GTG GAA ACA AAT CAG CAA TCT GAG AAA GAT AAC AAC ACT 728
 Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys Asp Asn Asn Thr
 195 200 205

TAT GAA AAC AGA AGA GTA CTT TCC AAC TAT GAA AGG CCA TAGAAACGTT 777
 Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg Pro
 210 215

TTAATTTTCA ATGAAGTCAC TGAAAATCCA ACTCCAGGAG CTATGGCAGT GTTAATGAAC 837
 ATATATCATC AGGTCTTAAA AAAAAAATAA AGGTAACTG AAAAGACAAC TGGCTACAAA 897
 GAAGGATGTC AGAATGTAAG GAACTATAA CTAATAGTCA TTACCAAAAT ACTAAAACCC 957

AACAAAATGC AACTGAAAAA TACCTTCCAA ATTTGCCAAG AAAAAAATT CTATTAACT 1017
AAAAAAAAAA AAAAAAAAAA AAA 1040

5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-22 -20 -15 -10
Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
-5 1 5 10
Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
15 20 25
Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
30 35 40
Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
45 50 55
Asp Gly Cys Lys Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu
60 65 70
Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
75 80 85 90
Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
95 100 105
Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
110 115 120
Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
125 130 135
Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
140 145 150
Ser Lys Ser Lys Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp
155 160 165 170
Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
175 180 185

55

Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
190 195 200

Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
205 210 215

Pro

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 45..767

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 111..767

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1013
(D) OTHER INFORMATION: /note= "nucleotides 1013 and 1014
are designated C, but may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG 56
Met Gly Thr Ala
-22 -20

AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT 104
Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe
-15 -10 -5

TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG 152
Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp
1 5 10

TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC 200
Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr
15 20 25 30

		TTC	TCC	GCA	ACC	GGA	TGC	CCT	TCT	GAG	CAA	CCA	ACA	TGC	CTG	TGG	TTT	248
		Phe	Ser	Ala	Thr	Gly	Cys	Pro	Ser	Glu	Gln	Pro	Thr	Cys	Leu	Trp	Phe	
						35					40					45		
5		CGC	TAC	GGT	GCT	CAC	CAG	CCT	GAG	AAC	CTG	TGC	TTG	GAC	GGG	TGC	AAA	296
		Arg	Tyr	Gly	Ala	His	Gln	Pro	Glu	Asn	Leu	Cys	Leu	Asp	Gly	Cys	Lys	
					50					55					60			
10		AGT	GAG	GCA	GAC	AAG	TTC	ACA	GTG	AGG	GAG	GCC	CTC	AAA	GAA	AAC	CAA	344
		Ser	Glu	Ala	Asp	Lys	Phe	Thr	Val	Arg	Glu	Ala	Leu	Lys	Glu	Asn	Gln	
				65					70					75				
15		GTT	TCC	CTC	ACT	GTA	AAC	AGA	GTG	ACT	TCA	AAT	GAC	AGT	GCA	ATT	TAC	392
		Val	Ser	Leu	Thr	Val	Asn	Arg	Val	Thr	Ser	Asn	Asp	Ser	Ala	Ile	Tyr	
			80					85					90					
		ATC	TGT	GGA	ATA	GCA	TTC	CCC	AGT	GTG	CCG	GAA	GCG	AGA	GCT	AAA	CAG	440
		Ile	Cys	Gly	Ile	Ala	Phe	Pro	Ser	Val	Pro	Glu	Ala	Arg	Ala	Lys	Gln	
			95				100					105				110		
20		ACA	GGA	GGA	GGG	ACC	ACA	CTG	GTG	GTA	AGA	GAA	ATT	AAG	CTG	CTC	AGC	488
		Thr	Gly	Gly	Gly	Thr	Thr	Leu	Val	Val	Arg	Glu	Ile	Lys	Leu	Leu	Ser	
						115					120				125			
25		AAG	GAA	CTG	CGG	AGC	TTC	CTG	ACA	GCT	CTT	GTA	TCA	CTG	CTC	TCT	GTC	536
		Lys	Glu	Leu	Arg	Ser	Phe	Leu	Thr	Ala	Leu	Val	Ser	Leu	Leu	Ser	Val	
					130					135					140			
30		TAT	GTG	ACC	GGT	GTG	TGC	GTG	GCC	TTC	ATA	CTC	CTC	TCC	AAA	TCA	AAA	584
		Tyr	Val	Thr	Gly	Val	Cys	Val	Ala	Phe	Ile	Leu	Leu	Ser	Lys	Ser	Lys	
				145					150					155				
35		TCC	AAC	CCT	CTA	AGA	AAG	AAA	GAA	ATA	AAA	GAA	GAC	TCA	CAA	AAG	AAG	632
		Ser	Asn	Pro	Leu	Arg	Lys	Lys	Glu	Ile	Lys	Glu	Asp	Ser	Gln	Lys	Lys	
				160				165					170					
40		AAG	AGT	GCT	CGG	CGT	ATT	TTT	CAG	GAA	ATT	GCT	CAA	GAA	CTA	TAC	CAT	680
		Lys	Ser	Ala	Arg	Arg	Ile	Phe	Gln	Glu	Ile	Ala	Gln	Glu	Leu	Tyr	His	
						175		180				185				190		
45		AAG	AGA	CAT	GTG	GAA	ACA	AAT	CAG	CAA	TCT	GAG	AAA	GAT	AAC	AAC	ACT	728
		Lys	Arg	His	Val	Glu	Thr	Asn	Gln	Gln	Ser	Glu	Lys	Asp	Asn	Asn	Thr	
						195				200					205			
50		TAT	GAA	AAC	AGA	AGA	GTA	CTT	TCC	AAC	TAT	GAA	AGG	CCA	TAGAAACGTT			777
		Tyr	Glu	Asn	Arg	Arg	Val	Leu	Ser	Asn	Tyr	Glu	Arg	Pro				
					210					215								
55		TTAATTTTCA	ATGAAGTCAC	TGAAAATCCA	ACTCCAGGAG	CTATGGCAGT	GTTAATGAAC											837
		ATATATCATC	AGGTCTTAAA	AAAAAATAA	AGGTAAACTG	AAAAGACAAC	TGGCTACAAA											897
		GAAGGATGTC	AGAATGTAAG	GAAACTATAA	CTAATAGTCA	TTACCAAAAT	ACTAAAACCC											957
		AACAAAATGC	AACTGAAAAA	TACCTTCCAA	ATTTGCCAAG	AAAAAAAATT	CTATTCCAAA											1017

20
 25
 30
 35

CTAAAAAAAAA AAAAAAAAAA AAAAA

1042

5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-22 -20 -15 -10

Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
-5 1 5 10

Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
15 20 25

Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
30 35 40

Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
45 50 55

Asp Gly Cys Lys Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu
60 65 70

Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
75 80 85 90

Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
95 100 105

Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
110 115 120

Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
125 130 135

Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
140 145 150

Ser Lys Ser Lys Ser Asn Pro Leu Arg Lys Lys Glu Ile Lys Glu Asp
155 160 165 170

Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
175 180 185

Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
 190 195 200

Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
 205 210 215

Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 37..750

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 103..750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACGCGTCC GGGAAAAGGC GGCACATGCA CCAGCG	ATG GGC CCT GTG AGC ACG	54
	Met Gly Pro Val Ser Thr	
	-22 -20	
AGC AGG AGG GGC CTC CGG CTA GGA ATC AGC CTG ATC CTT CTT CAA GTT		102
Ser Arg Arg Gly Leu Arg Leu Gly Ile Ser Leu Ile Leu Leu Gln Val		
-15 -10 -5		
GGT GTG GTG GGC GCC TGT ACT GTA TCT GTG CTA CAG CCA GGT TAC CTA		150
Gly Val Val Gly Ala Cys Thr Val Ser Val Leu Gln Pro Gly Tyr Leu		
1 5 10 15		
GAG GTG GAC TAC ACG TCT CAG ACT GTC ACC ATG GAG TGT ACC TTT TCT		198
Glu Val Asp Tyr Thr Ser Gln Thr Val Thr Met Glu Cys Thr Phe Ser		
20 25 30		
ACA ACT GGA TGC CCT GCA GTG CAA CCA AAA AGC TTG TGG TTT CGC TGT		246
Thr Thr Gly Cys Pro Ala Val Gln Pro Lys Ser Leu Trp Phe Arg Cys		
35 40 45		
GGC ACT CAC CAG CCT GAA GCT CTG TGC TTG GAC GGA TGC AGA AAT GAG		294
Gly Thr His Gln Pro Glu Ala Leu Cys Leu Asp Gly Cys Arg Asn Glu		
50 55 60		

	GCA GAC AAG TTC ACA GTG AAA GAA ACC CTG GAC CAG AAC CGA GTC TCC	342
	Ala Asp Lys Phe Thr Val Lys Glu Thr Leu Asp Gln Asn Arg Val Ser	
	65 70 75 80	
5	CTC ACT GTT AAC AGG CTG TCT CCA AAT GAC AGT GCA ATC TAC ATC TGT	390
	Leu Thr Val Asn Arg Leu Ser Pro Asn Asp Ser Ala Ile Tyr Ile Cys	
	85 90 95	
10	GGA ATA GCA TTT CCC AAT GAA CCG GTA CCA ACA GCC AAA CAG ACT GGA	438
	Gly Ile Ala Phe Pro Asn Glu Pro Val Pro Thr Ala Lys Gln Thr Gly	
	100 105 110	
	GAC GGG ACT ACA CTG GTG GTA AGA GAA AGA CTT TTC AGC AGG GAG GTG	486
	Asp Gly Thr Thr Leu Val Val Arg Glu Arg Leu Phe Ser Arg Glu Val	
15	115 120 125	
	CAC AGT CTC CTG ATA GTG CTC TTA GCA CTG CTC GCA GTC TAC GTC ACC	534
	His Ser Leu Leu Ile Val Leu Leu Ala Leu Leu Ala Val Tyr Val Thr	
	130 135 140	
20	GGT GTG TGT GTG ATC TTC ATA GTC CTC TTC AGA TCA AAA TCT AAC ACT	582
	Gly Val Cys Val Ile Phe Ile Val Leu Phe Arg Ser Lys Ser Asn Thr	
	145 150 155 160	
25	CCA AGA AGC AGA GAA ACC AAG GAA GAC TCG AAA AAG AAG AGT GCT CGA	630
	Pro Arg Ser Arg Glu Thr Lys Glu Asp Ser Lys Lys Lys Ser Ala Arg	
	165 170 175	
30	CGT ATC TTC CAG GAA ATT GCT CAA GAA TTA TAC CAT AAG AGA TAT GTG	678
	Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu Tyr His Lys Arg Tyr Val	
	180 185 190	
35	GAA ACA AGT CAT CAG CCT GAG CAA GAC GGC AAT TAT GAA AAC AGA AAA	726
	Glu Thr Ser His Gln Pro Glu Gln Asp Gly Asn Tyr Glu Asn Arg Lys	
	195 200 205	
40	GCA CTC CCC AGC CCT GGA AGA CCA TAGATGTGCT GACTTTTTAC TTAAACCATT	780
	Ala Leu Pro Ser Pro Gly Arg Pro	
	210 215	
45	GACAGTGCAA CTCCAGAATC TATGGCAGTG TGAATGGACA TACAGCAATC CAAACAACAG	840
	CAAAGAGAGC TGAGGTGTAG CTTGAGTGGC AAAGTGCTTG CCCAGTAGGC ATGAAGTCTT	900
	AGCTTTGATC CTCAGCACCA CATAACTCAG CAAAGTGACA CAAGCCTGTA TTCCCAACAT	960
	TGTGTAGTAG TATAAAAAGT CAGAAGTTCA AGGTCATCCC TGA CTATAGG ATGAACCTGA	1020
	AGTCAGAGAC ATGTTATCTT GTCTCAAAAA CACTGCCACC ACCAAGAGAA AAGGGCAGGA	1080
50	CAAGTGGGAA AACAGCCAGT CACGCCAGAA GGCAGAGCGG AAGTAACTGT CACGAACCAT	1140
	AATGATGGAA TGTGAAAACC TCAAGAAAAC TCAACTGGAG GACCTTTTTT CTAATTTTCC	1200
55	AGGAACAGTC TAAGGAGCCT CATTTTAAAG AAAA ACTTCA CCTTCAGCTT TTA	1253

(2) INFORMATION FOR SEQ ID NO:10:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15 Met Gly Pro Val Ser Thr Ser Arg Arg Gly Leu Arg Leu Gly Ile Ser
-22 -20 -15 -10

Leu Ile Leu Leu Gln Val Gly Val Val Gly Ala Cys Thr Val Ser Val
-5 1 5 10

20 Leu Gln Pro Gly Tyr Leu Glu Val Asp Tyr Thr Ser Gln Thr Val Thr
15 20 25

Met Glu Cys Thr Phe Ser Thr Thr Gly Cys Pro Ala Val Gln Pro Lys
30 35 40

25 Ser Leu Trp Phe Arg Cys Gly Thr His Gln Pro Glu Ala Leu Cys Leu
45 50 55

30 Asp Gly Cys Arg Asn Glu Ala Asp Lys Phe Thr Val Lys Glu Thr Leu
60 65 70

35 Asp Gln Asn Arg Val Ser Leu Thr Val Asn Arg Leu Ser Pro Asn Asp
75 80 85 90

40 Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Asn Glu Pro Val Pro
95 100 105

Thr Ala Lys Gln Thr Gly Asp Gly Thr Thr Leu Val Val Arg Glu Arg
110 115 120

45 Leu Phe Ser Arg Glu Val His Ser Leu Leu Ile Val Leu Leu Ala Leu
125 130 135

Leu Ala Val Tyr Val Thr Gly Val Cys Val Ile Phe Ile Val Leu Phe
140 145 150

Arg Ser Lys Ser Asn Thr Pro Arg Ser Arg Glu Thr Lys Glu Asp Ser
155 160 165 170

50 Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln Glu Leu
175 180 185

Tyr His Lys Arg Tyr Val Glu Thr Ser His Gln Pro Glu Gln Asp Gly
190 195 200

55

Asn Tyr Glu Asn Arg Lys Ala Leu Pro Ser Pro Gly Arg Pro
205 210 215

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..1290

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 112..1290

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 481
- (D) OTHER INFORMATION: /note= "may be T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 994
- (D) OTHER INFORMATION: /note= "may be A"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 49..51
- (D) OTHER INFORMATION: /note= "codon might be CGG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCCCCGGGCA GGTAGCGGCC GCTGAATTCT AGAACGCCCA CC ATG CCC CGG CAG	54
Met Pro Arg Gln	
-23 -20	
CTC AGC GCG GCG GCC GCG CTC TTC GCG TCC CTG GCC GTA ATT TTG CAC	102
Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala Val Ile Leu His	
-15 -10 -5	
GAT GGC AGT CAA ATG AGA GCA AAA GCA TTT CCA GAA ACC AGA GAT TAT	150
Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu Thr Arg Asp Tyr	
1 5 10	
TCT CAA CCT ACT GCA GCA GCA ACA GTA CAG GAC ATA AAA AAA CCT GTC	198
Ser Gln Pro Thr Ala Ala Ala Thr Val Gln Asp Ile Lys Lys Pro Val	
15 20 25	

5	CAG CAA CCA GCT AAG CAA GCA CCT CAC CAA ACT TTA GCA GCA AGA TTC Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu Ala Ala Arg Phe 30 35 40 45	246
10	ATG GAT GGT CAT ATC ACC TTT CAA ACA GCG GCC ACA GTA AAA ATT CCA Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr Val Lys Ile Pro 50 55 60	294
15	ACA ACT ACC CCA GCA ACT ACA AAA AAC ACT GCA ACC ACC AGC CCA ATT Thr Thr Thr Pro Ala Thr Thr Lys Asn Thr Ala Thr Thr Ser Pro Ile 65 70 75	342
20	ACC TAC ACC CTG GTC ACA ACC CAG GCC ACA CCC AAC AAC TCA CAC ACA Thr Tyr Thr Leu Val Thr Thr Gln Ala Thr Pro Asn Asn Ser His Thr 80 85 90	390
25	GCT CCT CCA GTT ACT GAA GTT ACA GTC GGC CCT AGC TTA GCC CCT TAT Ala Pro Pro Val Thr Glu Val Thr Val Gly Pro Ser Leu Ala Pro Tyr 95 100 105	438
30	TCA CTG CCA CCC ACC ATC ACC CCA CCA GCT CAT ACA ACT GGA ACC AGT Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr Thr Gly Thr Ser 110 115 120 125	486
35	TCA TCA ACC GTC AGC CAC ACA ACT GGG AAC ACC ACT CAA CCC AGT AAC Ser Ser Thr Val Ser His Thr Thr Gly Asn Thr Thr Gln Pro Ser Asn 130 135 140	534
40	CAG ACC ACC CTT CCA GCA ACT TTA TCG ATA GCA CTG CAC AAA AGC ACA Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu His Lys Ser Thr 145 150 155	582
45	ACC GGT CAG AAG CCT GTT CAA CCC ACC CAT GCC CCA GGA ACA ACG GCA Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro Gly Thr Thr Ala 160 165 170	630
50	GCT GCC CAC AAT ACC ACC CGC ACA GCT GCA CCT GCC TCC ACG GTT CCT Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala Ser Thr Val Pro 175 180 185	678
55	GGG CCC ACC CTT GCA CCT CAG CCA TCG TCA GTC AAG ACT GGA ATT TAT Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Val Lys Thr Gly Ile Tyr 190 195 200 205	726
60	CAG GTT CTA AAC GGA AGC AGA CTC TGT ATA AAA GCA GAG ATG GGG ATA Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala Glu Met Gly Ile 210 215 220	774
65	CAG CTG ATT GTT CAA GAC AAG GAG TCG GTT TTT TCA CCT CGG AGA TAC Gln Leu Ile Val Gln Asp Lys Glu Ser Val Phe Ser Pro Arg Arg Tyr 225 230 235	822

	TTC AAC ATC GAC CCC AAC GCA ACG CAA GCC TCT GGG AAC TGT GGC ACC	870
	Phe Asn Ile Asp Pro Asn Ala Thr Gln Ala Ser Gly Asn Cys Gly Thr	
	240 245 250	
5	CGA AAA TCC AAC CTT CTG TTG AAT TTT CAG GGC GGA TTT GTG AAT CTC	918
	Arg Lys Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly Phe Val Asn Leu	
	255 260 265	
10	ACA TTT ACC AAG GAT GAA GAA TCA TAT TAT ATC AGT GAA GTG GGA GCC	966
	Thr Phe Thr Lys Asp Glu Glu Ser Tyr Tyr Ile Ser Glu Val Gly Ala	
	270 275 280 285	
15	TAT TTG ACC GTC TCA GAT CCA GAG ACA ATT TAC CAA GGA ATC AAA CAT	1014
	Tyr Leu Thr Val Ser Asp Pro Glu Thr Ile Tyr Gln Gly Ile Lys His	
	290 295 300	
20	GCG GTG GTG ATG TTC CAG ACA GCA GTC GGG CAT TCC TTC AAG TGC GTG	1062
	Ala Val Val Met Phe Gln Thr Ala Val Gly His Ser Phe Lys Cys Val	
	305 310 315	
25	AGT GAA CAG AGC CTC CAG TTG TCA GCC CAC CTG CAG GTG AAA ACA ACC	1110
	Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln Val Lys Thr Thr	
	320 325 330	
30	GAT GTC CAA CTT CAA GCC TTT GAT TTT GAA GAT GAC CAC TTT GGA AAT	1158
	Asp Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp His Phe Gly Asn	
	335 340 345	
35	GTG GAT GAG TGC TCG TCT GAC TAC ACA ATT GTG CTT CCT GTG ATT GGG	1206
	Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu Pro Val Ile Gly	
	350 355 360 365	
40	GCC ATC GTG GTT GGT CTC TGC CTT ATG GGT ATG GGT GTC TAT AAA ATC	1254
	Ala Ile Val Val Gly Leu Cys Leu Met Gly Met Gly Val Tyr Lys Ile	
	370 375 380	
45	CGC CTA AGG TGT CAA TCA TCT GGA TAC CAG AGA ATC TAATTGTTGC	1300
	Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile	
	385 390	
50	CCGGGGGGAA TGAAATAAT GGAATTTAGA GAACTCTTTC ATCCTTCCAG GATGGATGTT	1360
	GGAAATTCCC TCAGAGTGTG GGTCTTCAA ACAATGTAAA CCACCATCTT CTATTCAAAT	1420
55	GAAGTGAGTC ATGTGTGATT TAAGTTCAGG CAGCACATCA ATTTCTAAAT ACTTTTTGTT	1480
	TATTTTATGA AAGATATAGT GAGCTGTTTA TTTTCTAGTT TCCTTTAGAA TATTTTAGCC	1540
	ACTCAAAGTC AACATTTGAG ATATGTTGAA TTAACATAAT ATATGTAAAG TAGAATAAGC	1600
	CTTCAAATTA TAAACCAAGG GTCAATTGTA ACTAATACTA CTGTGTGTGC ATTGAAGATT	1660
	TTATTTTACC CTTGATCTTA ACAAAGCCTT TGCTTTGTTA TCAAATGGAC TTTCAGTGCT	1720
	TTTACTATCT GTGTTTTATG GTTTCATGTA ACATACATAT TCCTGGTGTA GCACTTAACT	1780

5
10
15
20
25
30
35
40
45
50

CCTTTTCCAC TTTAAATTTG TTTTGTGTTTT TTGAGACGGA GTTTCACCTCT TGTCACCCAG 1840
GCTGGAGTAC AGTGGCACGA TCTCGGCTTA TGGCAACCTC CGCCTCCCGG GTTCAAGTGA 1900
TTCTCCTGCT TCAGCTTCCC GAGTAGCTGG GATTACAGGC ACACACTACC ACGCCTGGCT 1960
AATTTTTGTA TTTTATTAT AGACGGGGTT TCACCATGTT GGCCAGACTG GTCTTGAAGT 2020
CTTGACCTCA GGTGATCCAC CCACCTCAGC CTCCCAAAGT GCTGGGATTA CAGGCATGAG 2080
CCATTGCGCC CGGCCTTAAA TGTTTTTTTTT AATCATCAAA AAGAACAACA TATCTCAGGT 2140
TGTCTAAGTG TTTTATGTA AAACCAACAA AAAGAACAAA TCAGCTTATA TTTTTTATCT 2200
TGATGACTCC TGCTCCAGAA TCGCTAGACT AAGAATTAGG TGGCTACAGA TGGTAGAACT 2260
AAACAATAAG CAAGAGACAA TAATAATGGC CCTTAATTAT TAACAAAGTG CCAGAGTCTA 2320
GGCTAAGCAC TTTATCTATA TCTCATTICA TTCTCACAAC TTATAGGTGA ATGAGTAAAC 2380
TGAGACTTAA GGGAAGTGAA TCACTTAAAT GTCACCTGGC TAACTGATGG CAGAGCCAGA 2440
GCTTGAATTC ATGTTGGTCT GACATCAAGG TCTTTGGTCT TCTCCCTACA CCAAGTTACC 2500
TACAAGAACA ATGACACCAC ACTCTGCCTG AAGGCTCACA CCTCATACCA GCATACGCTC 2560
ACCTTACAGG GAAATGGGTT TATCCAGGAT CATGAGACAT TAGGGTAGAT GAAAGGAGAG 2620
CTTTGCAGAT AACAAAATAG CCTATCCTTA ATAAATCCTC CACTCTCTGG AAGGAGACTG 2680
AGGGGCTTTG TAAAACATTA GTCAGTTGCT CATTTTTATG GGATTGCTTA GCTGGGCTGT 2740
AAAGATGAAG GCATCAAATA AACTCAAAGT ATTTTTAAAT TTTTTTGATA ATAGAGAAAC 2800
TTCGCTAACC AACTGTTCTT TCTTGAGTGA TAGCCCCATC TTGTGGTAAC TTGCTGCTTC 2860
TGCACTTCAT ATCCATATTT CCTATTGTTC ACTTTATTCT GTAGAGCAGC CTGCCAAGAA 2920
TTTTATTTCT GCTGTTTTTT TTGCTGCTAA AGAAAGGAAC TAAGTCAGGA TGTTAACAGA 2980
AAAGTCCACA TAACCCTAGA ATTCTTAGTC AAGGAATAAT TCAAGTCAGC CTAGAGACCA 3040
TGTTGACTTT CCTCATGTGT TTCCTTATGA CTCAGTAAGT TGGCAAGGTC CTGACTTTAG 3100
TCTTAATAAA ACATTGAATT GTAGTAAAGG TTTTGTAAAT AAAAATTAC TTTGGAAAAA 3160
AAAAAAAAAA AA 3172

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Pro Arg Gln Leu Ser Ala Ala Ala Ala Leu Phe Ala Ser Leu Ala
 -23 -20 -15 -10
 Val Ile Leu His Asp Gly Ser Gln Met Arg Ala Lys Ala Phe Pro Glu
 -5 1 5
 Thr Arg Asp Tyr Ser Gln Pro Thr Ala Ala Ala Thr Val Gln Asp Ile
 10 15 20 25
 Lys Lys Pro Val Gln Gln Pro Ala Lys Gln Ala Pro His Gln Thr Leu
 30 35 40
 Ala Ala Arg Phe Met Asp Gly His Ile Thr Phe Gln Thr Ala Ala Thr
 45 50 55
 Val Lys Ile Pro Thr Thr Thr Pro Ala Thr Thr Lys Asn Thr Ala Thr
 60 65 70
 Thr Ser Pro Ile Thr Tyr Thr Leu Val Thr Thr Gln Ala Thr Pro Asn
 75 80 85
 Asn Ser His Thr Ala Pro Pro Val Thr Glu Val Thr Val Gly Pro Ser
 90 95 100 105
 Leu Ala Pro Tyr Ser Leu Pro Pro Thr Ile Thr Pro Pro Ala His Thr
 110 115 120
 Thr Gly Thr Ser Ser Ser Thr Val Ser His Thr Thr Gly Asn Thr Thr
 125 130 135
 Gln Pro Ser Asn Gln Thr Thr Leu Pro Ala Thr Leu Ser Ile Ala Leu
 140 145 150
 His Lys Ser Thr Thr Gly Gln Lys Pro Val Gln Pro Thr His Ala Pro
 155 160 165
 Gly Thr Thr Ala Ala Ala His Asn Thr Thr Arg Thr Ala Ala Pro Ala
 170 175 180 185
 Ser Thr Val Pro Gly Pro Thr Leu Ala Pro Gln Pro Ser Ser Val Lys
 190 195 200
 Thr Gly Ile Tyr Gln Val Leu Asn Gly Ser Arg Leu Cys Ile Lys Ala
 205 210 215
 Glu Met Gly Ile Gln Leu Ile Val Gln Asp Lys Glu Ser Val Phe Ser
 220 225 230

Pro Arg Arg Tyr Phe Asn Ile Asp Pro Asn Ala Thr Gln Ala Ser Gly
235 240 245

Asn Cys Gly Thr Arg Lys Ser Asn Leu Leu Leu Asn Phe Gln Gly Gly
250 255 260 265

Phe Val Asn Leu Thr Phe Thr Lys Asp Glu Glu Ser Tyr Tyr Ile Ser
270 275 280

Glu Val Gly Ala Tyr Leu Thr Val Ser Asp Pro Glu Thr Ile Tyr Gln
285 290 295

Gly Ile Lys His Ala Val Val Met Phe Gln Thr Ala Val Gly His Ser
300 305 310

Phe Lys Cys Val Ser Glu Gln Ser Leu Gln Leu Ser Ala His Leu Gln
315 320 325

Val Lys Thr Thr Asp Val Gln Leu Gln Ala Phe Asp Phe Glu Asp Asp
330 335 340 345

His Phe Gly Asn Val Asp Glu Cys Ser Ser Asp Tyr Thr Ile Val Leu
350 355 360

Pro Val Ile Gly Ala Ile Val Val Gly Leu Cys Leu Met Gly Met Gly
365 370 375

Val Tyr Lys Ile Arg Leu Arg Cys Gln Ser Ser Gly Tyr Gln Arg Ile
380 385 390